



PCT10

RAW SEQUENCE LISTING

DATE: 07/29/2002

PATENT APPLICATION: US/10/089,678

TIME: 08:47:14

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\07292002\J089678.raw

3 <110> APPLICANT: ASANO, Shinichiro
 5 <120> TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE
 PROTEIN, AND
 6 NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
 8 <130> FILE REFERENCE: Q68821
 10 <140> CURRENT APPLICATION NUMBER: 10/089,678
 C--> 11 <141> CURRENT FILING DATE: 2002-05-02
 13 <150> PRIOR APPLICATION NUMBER: JP 2000-236140
 14 <151> PRIOR FILING DATE: 2000-08-03
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06660
 17 <151> PRIOR FILING DATE: 2001-08-02
 19 <160> NUMBER OF SEQ ID NOS: 3
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1167
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Bacillus thuringiensis
 28 <400> SEQUENCE: 1
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 31 1 5 10 15
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 35 20 25 30
 38 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
 39 35 40 45
 42 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
 43 50 55 60
 46 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
 47 65 70 75 80
 50 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
 51 85 90 95
 54 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
 55 100 105 110
 58 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
 59 115 120 125
 62 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
 63 130 135 140
 66 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
 67 145 150 155 160
 70 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
 71 165 170 175
 74 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
 75 180 185 190
 78 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
 79 195 200 205

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82 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
83      210      215      220
86 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
87 225      230      235      240
90 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
91      245      250      255
94 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
95      260      265      270
98 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
99      275      280      285
102 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
103      290      295      300
106 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
107 305      310      315      320
110 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
111      325      330      335
114 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile
115      340      345      350
118 Glu Phe Tyr Thr Thr Arg Ala Gly Leu Pro Leu Asn Asn Thr Glu Tyr
119      355      360      365
122 Leu Glu Tyr Trp Val Gly His Ser Ile Lys Tyr Lys Asn Thr Asn Ala
123      370      375      380
126 Ser Ser Ala Leu Glu Arg Asn Tyr Gly Thr Ile Thr Ser Asn Lys Ile
127 385      390      395      400
130 Lys Tyr Tyr Asp Leu Ala Asn Lys Asp Ile Phe Gln Val Arg Ser Leu
131      405      410      415
134 Gly Ala Asp Leu Ala Asn Tyr Tyr Ala Gln Val Tyr Gly Val Pro Tyr
135      420      425      430
138 Ala Ser Phe Thr Leu Leu Asp Lys Asn Thr Gly Ser Gly Ser Val Gly
139      435      440      445
142 Gly Phe Thr Tyr Ser Lys Pro His Thr Thr Met Gln Val Cys Thr Gln
143      450      455      460
146 Asn Tyr Asn Thr Ile Asp Glu Ile Pro Pro Glu Asn Glu Pro Leu Ser
147 465      470      475      480
150 Arg Gly Tyr Ser His Arg Leu Ser His Ile Thr Ser Tyr Ser Phe Ser
151      485      490      495
154 Lys Asn Ala Ser Ser Pro Ala Arg Tyr Gly Asn Leu Pro Val Phe Ala
155      500      505      510
158 Trp Thr His Arg Ser Ala Asp Val Thr Asn Thr Val Tyr Ser Asp Lys
159      515      520      525
162 Ile Thr Gln Ile Pro Val Val Lys Ala His Thr Leu Val Ser Gly Thr
163      530      535      540
166 Thr Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asn Ile Leu Lys Arg
167 545      550      555      560
170 Thr Ser Ser Gly Pro Leu Ala Tyr Thr Ser Val Ser Val Lys Ser Pro
171      565      570      575
174 Leu Ser Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
175      580      585      590
178 Leu Arg Leu Phe Val Thr Ile Ser Gly Thr Arg Ile Tyr Ser Ile Asn

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179	595	600	605
182 Val Asn Lys Thr Met Asn Lys Gly Asp Asp Leu Thr Phe Asn Thr Phe			
183 610	615	620	
186 Asp Leu Ala Thr Ile Gly Thr Ala Phe Thr Phe Ser Asn Tyr Ser Asp			
187 625	630	635	640
190 Ser Leu Thr Val Gly Ala Asp Ser Phe Ala Ser Gly Gly Glu Val Tyr			
191 645	650	655	
194 Val Asp Lys Phe Glu Leu Ile Pro Val Asn Ala Thr Phe Glu Ala Glu			
195 660	665	670	
198 Glu Asp Leu Asp Val Ala Lys Lys Ala Val Asn Gly Leu Phe Thr Ser			
199 675	680	685	
202 Lys Lys Asp Ala Leu Gln Thr Ser Val Thr Asp Tyr Gln Val Asn Gln			
203 690	695	700	
206 Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Glu Leu Tyr Pro Asn Glu			
207 705	710	715	720
210 Lys Arg Met Leu Trp Asp Ala Val Lys Glu Ala Lys Arg Leu Val Gln			
211 725	730	735	
214 Ala Arg Asn Leu Leu Gln Asp Thr Gly Phe Asn Arg Ile Asn Gly Glu			
215 740	745	750	
218 Asn Gly Trp Thr Gly Ser Thr Gly Ile Glu Val Ala Glu Gly Asp Val			
219 755	760	765	
222 Leu Phe Lys Asp Arg Ser Leu Arg Leu Thr Ser Ala Arg Glu Ile Asp			
223 770	775	780	
226 Thr Glu Thr Tyr Pro Thr Tyr Leu Tyr Gln Gln Ile Asp Glu Ser Leu			
227 785	790	795	800
230 Leu Lys Pro Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Gly Ser Ser			
231 805	810	815	
234 Gln Asp Leu Glu Ile Lys Leu Ile Arg His Arg Ala Asn Gln Ile Val			
235 820	825	830	
238 Lys Asn Val Pro Asp Asn Leu Leu Pro Asp Val Leu Pro Val Asn Ser			
239 835	840	845	
242 Cys Gly Gly Ile Asp Arg Cys Ser Glu Gln Gln Tyr Val Asp Ala Asn			
243 850	855	860	
246 Leu Ala Leu Glu Asn Asn Gly Glu Asn Gly Asn Met Ser Ser Asp Ser			
247 865	870	875	880
250 His Ala Phe Ser Phe His Ile Asp Thr Gly Glu Ile Asp Leu Asn Glu			
251 885	890	895	
254 Asn Thr Gly Ile Trp Val Val Phe Lys Ile Pro Thr Thr Asn Gly Tyr			
255 900	905	910	
258 Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Glu Gly Pro Leu Ser Gly			
259 915	920	925	
262 Glu Thr Leu Glu Arg Ala Gln Gln Gln Glu Gln Gln Trp Gln Asp Lys			
263 930	935	940	
266 Met Ala Arg Lys Arg Gly Ala Ser Glu Lys Ala Tyr Tyr Ala Ala Lys			
267 945	950	955	960
270 Gln Ala Ile Asp Arg Leu Phe Ala Asp Tyr Gln Asp Gln Lys Leu Asn			
271 965	970	975	
274 Ser Gly Val Glu Met Ser Asp Met Leu Ala Ala Gln Asn Leu Val Gln			
275 980	985	990	

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278 Ser Ile Pro Tyr Val Tyr Asn Asp Ala Leu Pro Glu Ile Pro Gly Met
279      995      1000      1005
282 Asn Tyr Thr Ser Phe Thr Glu Leu Thr Asn Arg Leu Gln Gln Ala
283      1010      1015      1020
286 Trp Asn Leu Tyr Asp Leu Arg Asn Ala Ile Pro Asn Gly Asp Phe
287      1025      1030      1035
290 Arg Asn Gly Leu Ser Asp Trp Asn Ala Thr Ser Asp Val Asn Val
291      1040      1045      1050
294 Gln Gln Leu Ser Asp Thr Ser Val Leu Val Ile Pro Asn Trp Asn
295      1055      1060      1065
298 Ser Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Tyr Arg Tyr
299      1070      1075      1080
302 Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asp Gly Tyr
303      1085      1090      1095
306 Val Ile Ile Arg Asp Gly Ala Asn Gln Thr Glu Thr Leu Thr Phe
307      1100      1105      1110
310 Asn Ile Cys Asp Asp Asp Thr Gly Val Leu Ser Ala Asp Gln Thr
311      1115      1120      1125
314 Ser Tyr Ile Thr Lys Thr Val Glu Phe Thr Pro Ser Thr Glu Gln
315      1130      1135      1140
318 Val Trp Ile Asp Met Ser Glu Thr Glu Gly Val Phe Asn Ile Glu
319      1145      1150      1155
322 Ser Val Glu Leu Val Leu Glu Glu Glu
323      1160      1165
326 <210> SEQ ID NO: 2
327 <211> LENGTH: 3504
328 <212> TYPE: DNA
329 <213> ORGANISM: Bacillus thuringiensis
331 <220> FEATURE:
332 <221> NAME/KEY: exon
333 <222> LOCATION: (1)..(3501)
334 <223> OTHER INFORMATION:
337 <400> SEQUENCE: 2
338 atg agt cca aat aat caa aat gaa tat gaa att cta gat gct tca tca      48
339 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Leu Asp Ala Ser Ser
340 1      5      10      15
342 tct act tct gta tcc gat aat tct gtt aga tac cct tta gca aac gat      96
343 Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp
344      20      25      30
346 caa acg acc aca tta caa aac atg aac tat aaa gat tat ctg aga atg      144
347 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
348      35      40      45
350 tct gag gga gag aat cct gaa tta ttt gga aat ccg gag acg ttt att      192
351 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
352      50      55      60
354 agt tca tct acg gtt caa act gga att ggc att gtt ggt caa gta ctg      240
355 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
356 65      70      75      80
358 ggg gct tta ggg gtt cca ttt gct gga cag ata gct agt ttt tat agt      288

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359 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
360      85      90      95
362 ttc att gtc ggt caa tta tgg cca tca agt acc gtg agt gta tgg gaa      336
363 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
364      100      105      110
366 atg att atg aaa caa gtg gaa gat cta att gat caa aaa ata aca gat      384
367 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
368      115      120      125
370 tct gta agg aaa aca gcg ctt gca gga cta caa gga tta gga gat ggc      432
371 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
372      130      135      140
374 tta gac gta tat cag aaa tca ctt aag aat tgg ctg gaa aat cgt aat      480
375 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
376 145      150      155      160
378 gat aca aga gct aga agt gtt gtg gtg acc caa tat ata gct tta gag      528
379 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
380      165      170      175
382 ctt gat ttt gtt gct aaa atc cca tct ttt gca ata tct gga cag gaa      576
383 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
384      180      185      190
386 gta cca tta tta tca gtg tat gca caa gca gcg aat tta cat ttg cta      624
387 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
388      195      200      205
390 tta tta cga gat gct tcc att ttt gga gca gag tgg gga ttc aca cca      672
391 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
392      210      215      220
394 gga gaa att tcc aca ttt tat gat cgt cag gtg aca cgt acc gcc caa      720
395 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
396 225      230      235      240
398 tac tcg gat tat tgt gta aag tgg tat aac act ggc tta gat aaa tta      768
399 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
400      245      250      255
402 aaa ggt acg aat gct gca agt tgg ctg aag tat cac caa ttc cga aga      816
403 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
404      260      265      270
406 gaa atg aca tta ctg gta tta gat tta gta gcg tta ttt cca aac tat      864
407 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
408      275      280      285
410 gac aca cgt acg tat cca atc gaa aca acg gcc caa ctt aca cgg gaa      912
411 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
412      290      295      300
414 gtg tat aca gat cca ata gta ttt aac aga gaa aca agt ggt gga ttt      960
415 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
416 305      310      315      320
418 tgt agg cgt tgg tca ctt aac agt gat att tct ttt tca gaa gtc gaa      1008
419 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
420      325      330      335
422 agc gct gta att cgt tca cca cac cta ttt gat ata ctc agt gaa ata      1056
423 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date